Application No. 10/568,761 Amendment dated May 2, 2008 Reply to Office Action of December 3, 2007

AMENDMENTS TO THE SPECIFICATION

In the Specification

Please replace the paragraph at page 12, lines 8-23 with the following amended paragraph:

For example, a gene encoding a homologue of a human protein can include genes of different organisms such as a mouse and a rat, corresponding to the human gene encoding the protein. These genes (homologues) can be identified HomoloGene (http://www.ncbi.nlm.nih.gov/HomoloGene/). Specifically, a specific human base sequence is applied BLAST (Proc. Natl. Acad. Sci. USA 90:5873-5877, http://www.ncbi.nlm.nih.gov/BLAST/) to obtain an accession number of a coincident (Score is the highest, E-value is 0 and Identity indicates 100%) sequence. This accession number is inputted in UniGene (http://www.ncbi.nlm.nih.gov/UniGene/), and the obtained UniGene Cluster ID (number indicated at Hs.) is inputted in HomoloGene. HomoloGene and UniGene can be addressed at the website of the National center for Biotechnology Information of the National Library of Medicine, National Institutes of Health. From the resulting list showing a gene homologue correlation of genes of different organisms and the human gene, the genes of different organisms such as a mouse and a rat can be selected as genes (homologues) corresponding to the human gene indicated by the specific base sequence.

Please replace the paragraph at page 13, lines 12-25 and continuing on page 14, lines 1-5 with the following amended paragraph:

In the specification, the "protein" or the "(poly)peptide" includes not only a "protein" or a "(poly)peptide" indicated by a specific amino acid sequence (SEQ ID No: 2) but also its homologous species (homologues and splice variants), mutants, derivatives, mature substances, amino acid modified substances and the like so long as these are equal thereto in biological functions. Homologues here can include proteins of different organisms such as a mouse and a rat, corresponding to the human protein. They can be identified deductively from base sequences

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of genes identified by HomoloGene—(http://www.nebi.nlm.nih.gov/HomoloGene/). Mutants include alle-mutants present in nature, mutants not present in nature and mutants having amino acid sequences which are modified by artificial deletion, substitution, addition or insertion. Further, the mutants can include those which are homologous to proteins or (poly)peptides without mutation by at least 70%, preferably 80%, more preferably 95%, further preferably 97%. The amino acid modified substances include amino acid modified substances present in nature and amino acid modified substances not present in nature. Specifically, amino acid phosphates can be mentioned.